

Amendments to the Specification

Please amend the Specification as follows:

Please replace paragraph [0074] on page 16 lines 12-19 as follows:

[0074] The 684 genes of *B. subtilis* were subsequently clustered into five groups using k-means clustering. The Euclidean distance was used to measure the distance between genes, while the centroid of a cluster was defined by the median over all genes in the cluster. The number of clusters was chosen such that a significant overlap was avoided. The k-means algorithm was repeated 1,000,000 times starting from different random initial clusterings. The optimal solution was found 81 times. ~~The full clustering result is available at <http://bonsai.ims.u-tokyo.ac.jp/~mdchoon/publications/Subtilis/clusters.html>.~~